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PCT09

RAW SEQUENCE LISTING

DATE: 03/29/2002 P.S

PATENT APPLICATION: US/09/701,001B

TIME: 13:51:05

Input Set : A:\Asahilpc.app

Output Set: N:\CRF3\03292002\I701001B.raw

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3 <110> APPLICANT: ONO, MITSU HARU
4      SOKA, TAKAYUKI
5      MORIMOTO, IKUO
6      MIYAMURA, KOICHI
8 <120> TITLE OF INVENTION: CELL SEPARATION DEVICE AND SEPARATION METHOD
10 <130> FILE REFERENCE: ASAHI-1-PC-1
12 <140> CURRENT APPLICATION NUMBER: 09/701,001B
13 <141> CURRENT FILING DATE: 2000-11-22
15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02711
16 <151> PRIOR FILING DATE: 1999-05-24
18 <150> PRIOR APPLICATION NUMBER: JP 159957
19 <151> PRIOR FILING DATE: 1998-05-25
21 <150> PRIOR APPLICATION NUMBER: JP 163023
22 <151> PRIOR FILING DATE: 1998-05-26
24 <160> NUMBER OF SEQ ID NOS: 66
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 5
30 <212> TYPE: PRT
31 <213> ORGANISM: Mus sp.
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47 Gly
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51 <211> LENGTH: 9
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61 <211> LENGTH: 15
62 <212> TYPE: PRT
63 <213> ORGANISM: Mus sp.
65 <400> SEQUENCE: 4

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66 Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
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80 <210> SEQ ID NO: 6
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83 <213> ORGANISM: Mus sp.
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91 <211> LENGTH: 330
92 <212> TYPE: DNA
93 <213> ORGANISM: Mus sp.
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96 <221> NAME/KEY: CDS
97 <222> LOCATION: (1)..(330)
99 <400> SEQUENCE: 7
100 cct gag ctg gtg aag cct ggg gct tca gtg aag atg tcc tgc aag gct   48
101 Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala
102   1           5           10           15
104 tct gga tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga   96
105 Ser Gly Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg
106           20           25           30
108 act gga cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt   144
109 Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly
110           35           40           45
112 agt gct tac tac aat gag atg ttc aag ggc aag gcc aca ctg act gca   192
113 Ser Ala Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala
114           50           55           60
116 gac aaa tcc tcc aac aca gcc tac atg cag ctc agc agc ctg aca tct   240
117 Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
118   65           70           75           80
120 gag gac tct gcg gtc tat ttc tgt gca aga cgc gga act ggg acg ggg   288
121 Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly
122           85           90           95
124 ttt gct tac tgg ggc cga ggg act ctg gtc act gtc tct gca   330
125 Phe Ala Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala
126           100           105           110
129 <210> SEQ ID NO: 8
130 <211> LENGTH: 309
131 <212> TYPE: DNA
132 <213> ORGANISM: Mus sp.

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135 <221> NAME/KEY: CDS
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140 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys
141 1 5 10 15
143 gcc agc caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac 96
144 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr
145 20 25 30
147 caa cag aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc 144
148 Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser
149 35 40 45
151 aat cta gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg 192
152 Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
153 50 55 60
155 aca gac ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca 240
156 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala
157 65 70 75 80
159 acc tat tac tgt cag caa agt agt gag gat cct ccg acg ttc ggt gga 288
160 Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly
161 85 90 95
163 ggc acc aag ctg gaa atc aaa 309
164 Gly Thr Lys Leu Glu Ile Lys
165 100
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 925
170 <212> TYPE: DNA
171 <213> ORGANISM: Mus sp.
173 <220> FEATURE:
174 <221> NAME/KEY: CDS
175 <222> LOCATION: (1)..(915)
177 <400> SEQUENCE: 9
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179 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
180 1 5 10 15
182 gcc cag ccg gcc atg gcc gac att gtg ctg acc caa tct cca gct tct 96
183 Ala Gln Pro Ala Met Ala Asp Ile Val Leu Thr Gln Ser Pro Ala Ser
184 20 25 30
186 ttg gct gtg tct cta ggg cag agg gcc acc atc tcc tgc aag gcc agc 144
187 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser
188 35 40 45
190 caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac caa cag 192
191 Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln
192 50 55 60
194 aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc aat cta 240
195 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu
196 65 70 75 80
198 gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg aca gac 288

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199 Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
200      85      90      95
202 ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca acc tat 336
203 Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr
204      100      105      110
206 tac tgt cag caa agt agt gag gat cct ccg acg ttc ggt gga ggc acc 384
207 Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr
208      115      120      125
210 aag ctg gaa atc aaa ggt gga ggc ggt tca ggc gga ggt ggc tcc gga 432
211 Lys Leu Glu Ile Lys Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
212      130      135      140
214 ggt ggc gga tcg cag gtt cag ctg cag cag tct gga cct gag ctg gtg 480
215 Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val
216 145      150      155      160
218 aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac aca 528
219 Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr
220      165      170      175
222 ttc act gac tat gtt ata aac tgg ttg aac cag aga act gga cag ggc 576
223 Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly
224      180      185      190
226 ctt gag tgg att gga gag att tat cct gga agt ggt agt gct tac tac 624
227 Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr
228      195      200      205
230 aat gag atg ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc 672
231 Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
232      210      215      220
234 aac aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg 720
235 Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
236 225      230      235      240
238 gtc tat ttc tgt gca aga cgc gga act ggg acg ggg ttt gct tac tgg 768
239 Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp
240      245      250      255
242 ggc cga ggg act ctg gtc act gtc tct gca gcg gcc gca gac tac aag 816
243 Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Ala Asp Tyr Lys
244      260      265      270
246 gat gac gat gac aaa ggc tcg agc gag cag aag ctg atc agc gaa gag 864
247 Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu
248      275      280      285
250 gat ctg ggc tcg agg tcg acc cac cat cat cat cac cac ggg tcg acc 912
251 Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr
252      290      295      300
254 aaa tgataagctt 925
255 Lys
256 305
259 <210> SEQ ID NO: 10
260 <211> LENGTH: 925
261 <212> TYPE: DNA
262 <213> ORGANISM: Mus sp.
264 <220> FEATURE:

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270 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
271 1 5 10 15
273 gcc cag ccg gcc atg gcc cag gtt cag ctg cag cag tct gga cct gag 96
274 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu
275 20 25 30
277 ctg gtg aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144
278 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly
279 35 40 45
281 tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga act gga 192
282 Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly
283 50 55 60
285 cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt agt gct 240
286 Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala
287 65 70 75 80
289 tac tac aat gag atg ttc aag ggc aag gcc aca ctg act gca gac aaa 288
290 Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
291 85 90 95
293 tcc tcc aac aca gcc tac atg cag ctc agc agc ctg aca tct gag gac 336
294 Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
295 100 105 110
297 tct gcg gtc tat ttc tgt gca aga cgc gga act ggg acg ggg ttt gct 384
298 Ser Ala Val Tyr Phe Cys Ala Arg Gly Thr Gly Thr Gly Phe Ala
299 115 120 125
301 tac tgg ggc cga ggg act ctg gtc act gtc tct gca ggt gga ggc ggt 432
302 Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly
303 130 135 140
305 tca ggc gga ggt ggc tcc gga ggt ggc gga tgc gac att gtg ctg acc 480
306 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr
307 145 150 155 160
309 caa tct cca gct tct ttg gct gtg tct cta ggg cag agg gcc acc atc 528
310 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile
311 165 170 175
313 tcc tgc aag gcc agc caa agt gtt gat tat gat ggt gat agt tat atg 576
314 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met
315 180 185 190
317 aac tgg tac caa cag aaa cca gga cag cca ccc aaa ctc ctc atc tat 624
318 Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
319 195 200 205
321 gct gca tcc aat cta gaa tct ggg atc cca gcc agg ttt agt ggc agt 672
322 Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
323 210 215 220
325 ggg tct ggg aca gac ttc acc ctc aac atc cat cct gtg gag gag gag 720
326 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu
327 225 230 235 240
329 gat gct gca acc tat tac tgt cag caa agt agt gag gat cct ccg acg 768

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/701,001B

DATE: 03/29/2002

TIME: 13:51:06

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Output Set: N:\CRF3\03292002\I701001B.raw

L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15